

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: September 11, 2005, 01:49:24 ; Search time 291 Seconds

(without alignments) 8603.104 Million cell updates/sec

Title: US-10-664-958-4_COPY_73_1602
 Perfect score: 1530
 Sequence: atgaccaaaaggagggtgcct.....acaaggaatttgcagatttc 1530

Scoring table: IDENTITY_NUC

GapOp 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Post-processing: Minimum Match 0%

Maximum Match 100%
 Listing first 45 summaries

Issued_Patents_NA:*

1: /cgn2_6/podata/1/ina/5A_COMB.seq:*

2: /cgn2_6/podata/1/ina/5B_COMB.seq:*

3: /cgn2_6/podata/1/ina/6A_COMB.seq:*

4: /cgn2_6/podata/1/ina/6B_COMB.seq:*

5: /cgn2_6/podata/1/ina/PETUS_COMB.seq:*

6: /cgn2_6/podata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1 146.6 9.6 876 4 US-09-248-796A-5370 Sequence 5370, Ap

Sequence 5, Appli

Sequence 1, Appli

Sequence 8, Appli

Sequence 3, Appli

Sequence 5371, Ap

Sequence 1, Appli

Sequence 5384, Ap

Sequence 5383, Ap

Sequence 5065, Ap

Sequence 5153, Ap

Sequence 3, Appli

Sequence 798, Ap

Sequence 7915, Ap

Sequence 2, Appli

Sequence 1, Appli

Sequence 5372, Ap

Sequence 5373, Ap

Sequence 137, Ap

Sequence 109, Ap

Sequence 5091, Ap

Sequence 5317, Ap

Sequence 124276, Ap

Sequence 15238, A

Sequence 12111, A

Sequence 25318, A

Sequence 124277, A

Sequence 17037, A

ALIGNMENTS

RESULT 1
 Sequence 5370, Application US/09248796A.

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248-796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO: 5370

LENGTH: 876

TYPE: DNA

ORGANISM: Candida albicans

FEATURE:

NAME/KEY: unsure

LOCATION: (35)

OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unl

US-09-248-796A-5370

Query Match Similarity 9.6%; Score 146.6; DB 4; Length 876;

Best Local Similarity 52.2%; Pred. No. 1.7e-41;

Matches 385; Conservative 0; Mismatches 334; Indels 18; Gaps 2;

Sequence 5371, Ap

Sequence 5384, Ap

Sequence 5383, Ap

Sequence 5065, Ap

Sequence 5153, Ap

Sequence 3, Appli

Sequence 798, Ap

Sequence 7915, Ap

Sequence 2, Appli

Sequence 1, Appli

Sequence 5372, Ap

Sequence 5373, Ap

Sequence 137, Ap

Sequence 109, Ap

Sequence 5091, Ap

Sequence 5317, Ap

Sequence 124276, Ap

Sequence 15238, A

Sequence 12111, A

Sequence 25318, A

Sequence 124277, A

Sequence 17037, A

Sequence 12106, A

Sequence 14033, A

Sequence 12777, A

Sequence 23, Appli

Sequence 23, Appli

Sequence 9309, A

Sequence 14645, A

Sequence 14646, A

Sequence 14364, A

Sequence 8976, Ap

Sequence 1, Appli

Sequence 3, Appli

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Om nucleic - nucleic search, using sw model

Run on: September 11, 2005, 03:55:19 ; Search time 981 Seconds
(without alignments) 1 10242.485 Million cell updates/sec

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Title: US-10-664-958-4_COPY_73_1602
Perfect score: 1530
Sequence: 1 atgaccaaaaggagggtgcct.....acaaggaattgcagatttc 1530

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA,*

1: /cgn2_6/ptodata/1/pubpna/us07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/us06_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/us07_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/us07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/PCOM_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/us08_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/us09_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/us09c_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/us09c_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/us09c_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/us09c_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/us09c_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/us10c_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/us10c_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/us10c_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/us10c_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/us10c_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/us10c_PUBCOMB.seq:*

20: /cgn2_6/ptodata/1/pubpna/us10c_PUBCOMB.seq:*

21: /cgn2_6/ptodata/1/pubpna/us10c_PUBCOMB.seq:*

22: /cgn2_6/ptodata/1/pubpna/us10c_PUBCOMB.seq:*

23: /cgn2_6/ptodata/1/pubpna/us11c_PUBCOMB.seq:*

24: /cgn2_6/ptodata/1/pubpna/us11c_PUBCOMB.seq:*

25: /cgn2_6/ptodata/1/pubpna/us10c_PUBCOMB.seq:*

26: /cgn2_6/ptodata/1/pubpna/us10c_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
1	1530	100.0	1679	Sequence 4, Appli
2	787.6	51.5	1916	Sequence 2, Appli
3	787.6	51.5	3383	Sequence 1, Appli
4	184.6	12.1	707	Sequence 448, Appli
5	119.2	7.8	1656	Sequence 11096, Appli
6	117.6	7.7	1807	Sequence 3262, Appli
7	117.6	7.7	1948	Sequence 5515, Appli

ALIGNMENTS

RESULT 1
US-10-664-958-4
; Sequence 4, Application US/1064958
; Publication No. US2004021963A1
; GENERAL INFORMATION:
; APPLICANT: KOBUCHI, KYOKO
; APPLICANT: NINOMIYA, DAIKI
; APPLICANT: KOJIMA, MARI
; APPLICANT: UEDA, YOICHI
; APPLICANT: MARIYAMA, JUN-ICHI
; APPLICANT: KITAMOTO, KATSURAKI
; TITLE OF INVENTION: NEW AMINOPEPTIDASE AND THE GENES THEREOF
; FILE REFERENCE: 241461US0001
; CURRENT APPLICATION NUMBER: US/10/664,958
; PRIORITY APPLICATION NUMBER: PCT/JP02/02476
; PRIORITY FILING DATE: 2002-03-15
; PRIORITY APPLICATION NUMBER: JP 2001-078930
; PRIORITY FILING DATE: 2001-03-19
; PRIORITY APPLICATION NUMBER: JP 2001-293348
; PRIORITY FILING DATE: 2003-09-22
; PRIORITY FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 4
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
; FEATURE: NAME/KEY: CDS
; LOCATION: (73) . (1602)

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OM nucleic - nucleic search, using SW model

Run on: September 11, 2005, 01:46:04 ; Search time 4629 Seconds

(without alignments) 12581.191 Million cell updates/sec

Title: US-10-664-958-4_COPY_-73_-1602

Perfect score: 1530

Sequence: 1 atgaccacaaaggatgtctc.....acaagaaatgcagattc 1530

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_htc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gb81:*

9: gb_gb82:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	482	31.5	636	7 CO150272
2	453.4	29.6	684	7 CO136018
3	419.8	27.4	898	7 CO005654
4	409.4	26.8	901	7 CO013013
5	380.6	25.0	827	7 CO005655
6	352	23.0	780	7 CO009866
7	320.8	21.0	859	7 CO013014
8	316.4	20.7	535	1 A1211309
9	277.4	18.1	530	1 A1211331
10	255.4	16.8	764	6 CD495799
11	247.6	16.2	759	7 CB903053
12	247.4	16.2	691	7 CF873032
13	231	15.1	768	9 CL58944
14	215	14.1	391	5 BQ499748
15	211.2	13.8	828	2 BE643133
16	210.2	13.7	434	7 CN249799
17	195.6	12.8	539	1 A1211330
18	184.6	12.1	1030	7 CN249531
19	171.6	11.2	758	7 CN240819
20	167.4	10.9	915	7 CP831173
21	159.2	10.4	519	5 BQ505674
22	154.4	10.1	734	7 CP883059
23	10.0	571	9 CL552297	OB_Ba001
24	153	10.0	580	7 CN249701

RESULTS

REFERENCE	1 (bases 1 to 636)
AUTHORS	Yu, J., Whirel, W.C.A., Nieman, W.C., Bhatnagar, D. and Cleveland, T.B.
TITLE	Aspergillus flavus expressed sequence tags for identification of genes with putative roles in aflatoxin contamination of crops
JOURNAL	FEMS Microbiol. Lett. (#004) In press
COMMENT	Contact: Yu J, Food and Feed Safety Research Unit, USDA/ARS, Southern Regional Research Center, 1100 Robert E. Lee Boulevard, New Orleans, LA 70124, USA
FOOD AND FEED	Tel: 504 286 4405
SAFETY	Fax: 504 286 4419
RESEARCH	Email: Jiuyu@brrc.ars.usda.gov
UNIT	Contact: Dr. Yu at USDA/ARS, SRRC (jiuyu@brrc.ars.usda.gov) for clone information
SOUTHERN REGIONAL	PCR PRIMERS
RESEARCH CENTER	FORWARD: M13F
LA 70124, USA	BACKWARD: M13R
	Seq primer: M13 Forward
	PolyA+R.
	FEATURES
	source

LOCATIONS

Qualifiers

Organism="Aspergillus flavus"

MolType="mRNA"

Strain="NRRL 3357"

DbXref="taxon:5059"

Clone="NAG835"

Sex="asexual mycelia"

CellType="mycelia"

DevStage="developmental stages from 18 to 96 hours"

LabHost="E. coli DH10B T1 resistant cells"

CloneLib="Aspergillus flavus Normalized cDNA Expression Library"

Note="Vector: pBlueScript (SK+) (Stratagene), antibiotic selection marker: Carbenicillin; Site 1: NotI, at the 5 prime end; Site 2: EcoRI, at the 3 prime end; This

ALIGNMENTS

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OM nucleic - nucleic search, using sw model
 Run on: September 11, 2005, 01:45:05 ; Search time 6488 Seconds
 (without alignments) 11426.708 Million cell updates/sec

Title: US-10-664-958-4_COPY_73_1602

Perfect score: 1530

Sequence: 1 atgaccacaaaggagggtgcct.....acaaggaatggcagatttc 1530

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank:*

1: gb_ba:*

2: gb_hhg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pa:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description
1	1530	100.0	1679	BD178569
2	787.6	51.5	1916	BD178568
3	787.6	51.5	3383	BD178567
4	348.8	22.8	53380	NCB13020
5	348.8	22.8	65076	NCB13020
6	305.2	19.9	10000	CR382129_14
7	264.4	17.3	10000	CR382057_08
8	230.8	15.1	10000	CR382133_27
9	228.6	14.9	10000	CR382128_07
10	198.2	13.0	10000	CR382126_12
11	191.6	12.5	1891	6 I06495
12	191.6	12.5	10806	M25548
13	191.6	12.5	1891	8 YSCYLAP4A
14	191.6	12.5	2688	8 SCYKL103C
15	191.6	12.5	3557	8 SCHAPLAP
16	185.2	12.1	2053	8 SCAPL
17	183.8	12.0	11000	8 CR382139_01
18	183.8	12.0	11000	8 CR382139_02
19	156.4	10.2	11000	8 AB016815_3

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OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 00:43:58 ; Search time 808 Seconds

(without alignments) 11209.411 Million cell updates/sec

Title: US-10-664-958-4_COPY_73_1602
 perfect score: 1530

Sequence: atgaccaaaaggagtgtcct.....acaaggaaattgcagatttc 1530

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04;*

1: geneseqn1980s;*
 2: geneseqn1990s;*
 3: geneseqn2000s;*
 4: geneseqn2001as;*
 5: geneseqn2001bs;*
 6: geneseqn2002as;*
 7: geneseqn2002bs;*
 8: geneseqn2003as;*
 9: geneseqn2003bs;*
 10: geneseqn2003cs;*
 11: geneseqn2003ds;*
 12: geneseqn2004as;*
 13: geneseqn2004bs;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description	ALIGMENTS
1	1530	100.0	1679	AAL50169	RESULT 1 AAL50169 ID AAL50169 standard; DNA; 1679 BP.
2	787.6	51.5	1916	AAL50168	XX AAL50168 A nidulans
3	787.6	51.5	3383	AAL50167	XX AAL50167 A nidulans
4	758.4	49.6	858	ABZ51046	XX ABZ51046 Aspergillus
5	474.4	31.0	474	ADG38093	ADG38093 Aspergillus
6	191.6	12.5	1891	AAQ05601	AAQ05601 Gene encodes Aaf07925 Fusarium
7	184.6	12.1	707	AAF07925	Aaf07925 Fusarium Aaf0600 Mouse ami
8	114.8	7.5	1637	AAK90598	AAK90598 Human ami
9	112.8	7.4	1777	ADL4807	Adi24807 Intestina
10	109.2	7.1	1637	AAH14938	Ahh14938 Human cDNA
11	109.2	7.1	1671	AAH14938	Ahh14938 Human cDNA
12	109.2	7.1	1696	ADE31712	Ade31712 Human 816
13	109.2	7.1	1696	ACN7834	Acn7834 Tumour-as
14	109.2	7.1	1696	ADP9069	Adp9069 Human pro
15	109.2	7.1	1910	AML46727	Aal16727 Human pro
16	109.2	7.1	1990	ADP8286	Adp8286 Human MDD
17	109.2	7.1	2583	ABV28070	Abv28070 Human pro
18	109.2	7.1	2583	ABV28070	Abv28070 Human pro
19	107.6	7.0	1668	ADQ84787	Adq84787 Human tum
20	107.6	7.0	2264	AAH16161	Aah16161 Human cDNA

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 11, 2005, 15:11:49 ; Search time 125.5 Seconds
(without alignments) 9617.214 Million cell updates/sec

title: US-10-664-958-4_COPY_73_1602

Perfect score: 2784

Sequence: 1 atgaccaaaagggatgtcc.....acaaggaatttgcagatttc 1530

Scoring table: BLOSUM62

Xgapop	10.0	Xgapext	0.5
Ygapop	6.0	Ygapext	7.0
DelOp	6.0	Delect	7.0

Searched: 177461 seqs, 394431504 residues

Total number of hits satisfying chosen parameters: 3554922

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*
Maximum Match 100*
Listing first 45 summaries

Command line parameters:

```

-MODEL=frame+n2p model -DEV=x1P
-Q/-cgn2/1-USPFCO_spool_P/US0664958/runat_10092005_173357_2052/app_query.fasta
-DB=Published Applications AA -QWTF=fastan -SUFFIX=top20_Frapb -MINNTRCH=0.1
-LOOPCH=0 -LOOPEXT=0 -UNITS=1 -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=PCT -THR MAX=100
-TTR MIN=0 -ALIGNM=20 -MODE=LOCAL -OUTTYPE=ptc -NORM=exact -HEARSHZ=500 -MINLEN=-
-MAXLEN=2000000000 -USR=US0664958@runat_11_130@runat_10092005_173357_2052
-NCPU=6 -ICPPI=3 -NO_MMAR -LARGEROVERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAROP=10 -XGAPEXT=0.5
-XGAROP=6 -FCAPOF=7 -YGAPOF=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

```

Database :

```

1: /cgn2_6_ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6_ptodata/1/pubpaa/PCT_NW_PUB.pep:*
3: /cgn2_6_ptodata/1/pubpaa/US06_PUBCOMB.pep:*
4: /cgn2_6_ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6_ptodata/1/pubpaa/US07_NW_PUB.pep:*
6: /cgn2_6_ptodata/1/pubpaa/PCT_NW_PUBCOMB.pep:*
7: /cgn2_6_ptodata/1/pubpaa/US08_NW_PUB.pep:*
8: /cgn2_6_ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6_ptodata/1/pubpaa/US09_NW_PUBCOMB.pep:*
10: /cgn2_6_ptodata/1/pubpaa/US09_B_PUBCOMB.pep:*
11: /cgn2_6_ptodata/1/pubpaa/US09_C_PUBCOMB.pep:*
12: /cgn2_6_ptodata/1/pubpaa/US09_NW_PUBCOMB.pep:*
13: /cgn2_6_ptodata/1/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6_ptodata/1/pubpaa/US10_C_PUBCOMB.pep:*
15: /cgn2_6_ptodata/1/pubpaa/US10_D_PUBCOMB.pep:*
16: /cgn2_6_ptodata/1/pubpaa/US10_D_PUBCOMB.pep:*
17: /cgn2_6_ptodata/1/pubpaa/US10_E_PUBCOMB.pep:*
18: /cgn2_6_ptodata/1/pubpaa/US10_NW_PUBCOMB.pep:*
19: /cgn2_6_ptodata/1/pubpaa/US11_PUBCOMB.pep:*
20: /cgn2_6_ptodata/1/pubpaa/US11_NW_PUBCOMB.pep:*
21: /cgn2_6_ptodata/1/pubpaa/US10_NW_PUBCOMB.pep:*
22: /cgn2_6_ptodata/1/pubpaa/US10_PUBCOMB.pep:*

```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM nucleic - protein search, "using frame_plus_n2p mode"

Run on: September 11, 2005, 14:45:13 ; Search time 37 Seconds

(without alignments) 6173.679 Million cell updates/sec

Title: US-10-664-958-4_COPY_73_1602

Perfect score: 2784

Sequence: 1 argacccaaaggaggcgcc... acaagaatggcaggatttc 1530

Scoring table: BLOSUM62

Xgapop 10.0 , xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODUL=frame+n2p.model -DEV=xlp

-Q=/cgn2_1/USPTO_spool/r/US10664958/runat_10092005_173356_1993/app_query.fasta_1.1671

-DB=ISSUED_PATENTS_AA -QFORMAT=fasta -SUFFIX=top20.fil -MINMATCH=0.1 -LOOPCL=0

-LOPBXT=0 -UNITS=512 -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human0.cdi

-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=10 -THR MIN=0 -ALIGN=20

-MODE=LOCAL -OUTFORMAT=PTO -NORM=ext -REHPSPU=500 -MINLEN=0 -MAXLEN=2000000000

-NO_PMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPBXT=7 -YGAPOP=10 -YGAPBXT=0 -DBOP=6 -DELEXT=7

Database : Issued Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMBO.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMBO.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMBO.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMBO.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMBO.pep:*

6: /cgn2_6/ptodata/1/iaa/backfile1..pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1

US-09-538-092-495

; Sequence 495, Application US/09538092

; Patent No. 5753314

; GENERAL INFORMATION:

; APPLICANT: GLOT, Loic

; APPLICANT: Mansfield, Traci A.

; FILE REFERENCE: 15966-542

; CURRENT APPLICATION NUMBER: US/09-538,092

; CURRENT FILING DATE: 2000-03-29

; PRIORITY FILING DATE: 1999-04-01

; PRIORITY APPLICATION NUMBER: 60/178,965

; PRIORITY FILING DATE: 2000-02-01

; NUMBER OF SEQ ID NOS: 1387

; SOFTWARE: CurapatSeqFormatter Version 0.9

; SEQ ID NO: 495

; LENGTH: 514

; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae

; FEATURE:

; NAME/KB: misc_feature

; LOCATION: (0)..(0)

; OTHER INFORMATION: Polypeptide Accession Number YKL103C

US-09-538-092-495

; Alignment Scores:

; Pred. No.:

; Sequence 495, App

; Sequence 2, App1

; Sequence 4, App1

; Sequence 2, App1

; Sequence 6, App1

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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 11, 2005, 05:18:03 ; Search time 158.5 seconds
 (without alignments) 9886.198 Million cell updates/sec

Title: US-10-664-958-4_COPY_73_1602

Perfect score: 2784

Sequence: 1 atgaccaaaaggatgtcct.....acaagaattcagatttc 1530

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

```
-MODB=frame+, n2p.model -DEV=xlp
-Q=cfgn2_1/USP10_spool/p/US10664958/runat10092005_173355_1973/app_query.fasta_1.1671
-DB=UniProt_0 -OFMT=fatcat -SUPRTX=top20.rup -MINMATCH=0.1 -LOOPCT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=55 -DOCALIGN=200 -THR SCOREPCT=90 -THR MIN=0 -ALIGN=20
-MODE=LOCAL -OUTFMT=pfo -NORM=ext -HEA_SIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10664958 @CON_1 -1-153 @runat10092005_173355_1973 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NSIG SCORES=0 -WAIT=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : UniProt 03-*
 1: uniprot_sprot;*
 2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	1528	54.9	535	09HE85
2	1174	42.2	493	06CC01
3	1040	37.4	509	06FMP2
4	1034.5	37.2	519	06CK48
5	1013.5	36.4	514	1 AMPL YEAST
6	1006	36.1	506	2 06BJH6
7	998	35.8	469	2 06C022
8	907.5	32.6	498	2 075DQ2
9	883.5	31.7	476	2 06CPM9
10	867	31.1	495	2 096TK5
11	865.5	31.1	499	2 06CMC5
12	862.5	31.0	523	2 06BKU6
13	858	30.8	493	2 06BHZ6
14	857	30.8	484	2 06FR33
15	856	30.7	484	2 07RYK7
16	843	30.3	490	1 DNPE YEAST

RESULT 1		ALIGNMENTS	
ID	Q9HRS5	PRELIMINARY	PRT: 535 AA.
AC	Q9HRS5;		
DT	01-MAR-2001 (Tremblrel. 16, Created)		
DT	01-MAR-2001 (Tremblrel. 16, Last sequence update)		
DR	Related to aminopeptidase yuci, vacuolar. Name: B13020_180;		
DR	Neurospora crassa.		
OS	Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;		
OC	Sordariomycetidae; Sordariales; Sordariaceae; Neurospora;		
OX	NCBI-TaxID=5141;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Schnute U., Algn V., Hoheisel J., Brandt P., Fartmann B., Holland R.,		
RA	Nakatura G., Mewes H.W., Mannhaupt G.;		
RA	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.		
RL	[2]		
RP	SEQUENCE FROM N.A.		
RA	German Neurospora genome project;		
RL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AL451015; CAC18208; 1; -.		
DR	GO; GO:0005773; C-vacuole; IEA.		
DR	GO; GO:0004250; F-aminopeptidase I activity; IEA.		
DR	GO; GO:0006508; F-aminopeptidase I activity; peptidolysis; IEA.		
DR	InterPro: IPR001948; Peptidase_M18.		
DR	PFAM: PF02127; Peptidase_M18; 1.		
DR	PRINTS: PR00332; AMINOPTASE.		
KW	Aminopeptidase.		
SQ	SEQUENCE 555 AA: 58137 MN: 469P22A535396798 CRC64: Alignment Scores: Pred. No.: 4.3e-102 Score: 1528.00 Percent Similarity: 72.35% Best Local Similarity: 57.77% Query Match: 54.89% Gaps: 5		
	Length: 535 Matches: 305 Conservative: 77 Mismatches: 119 Indels: 27		

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OM nucleic - protein search, using frame_plus_n2p model
Run on: September 11, 2005, 14:11:55 ; Search time 41.5 Seconds
(without alignments)

7094.537 Million cell updates/sec
US-10-664-958-4_COPY_73_1602

Title: perfect score: 2784
Sequence: atgaccaaaaggagtgtccat.....acaaggaaattgcagatcc 1530

Scoring table: BLOSUM62
Xgapop 10.0 , xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Egapop 6.0 , Egapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

```
-MODEL:frame+ n2p.model -DEV=x1P
-Q=/sgn2/_USPRO.spool_p/_US10664958/runat_10092005_173355_1981/app_query.fasta_1.1671
-DB=PIR_79 -QFM=Fastaa -SUFFIX20=rpr -MINMATCH=0.1 -LOOPC=0 -LOOPEXT=0
-UNITS=51b -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40_cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGNC=20 -MODE=LOCAL
-OUTFMT=sto -NORM=ext -HARISIZE=500 -MINLEN=0 -MAXLEN=2000000000 -ICPU=3
-NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=700 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAEEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DSELEXT=7
```

Database : PIR_79:*

```
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1013.5	36.4	514 2 A33879	aminopeptidase yaci (EC 3.4.11.-) precursor, vacuolar - yeast (Saccharomyces cerevisiae)
2	843	30.3	490 2 A33879	aminopeptidase yaci (EC 3.4.11.-) precursor, vacuolar - yeast (Saccharomyces cerevisiae)
3	814.5	29.3	467 2 T38955	hypothetical prote
4	718	25.8	526 2 T49467	probable aspartyl aminopeptidase
5	677	24.3	429 2 A82340	aspartyl aminopept
6	650.5	23.4	392 2 T43206	probable aminopept
7	640	23.0	433 2 F96974	aspartyl aminopept
8	640	23.0	470 2 T15946	hypothetical prote
9	542.5	19.5	443 2 H87185	aminopeptidase I
10	486	17.5	433 2 A70336	probable PEP C prot
11	485.5	17.4	432 2 T36382	probable aminopept
12	464.5	16.0	423 2 B70178	vacuolar X-prolyl
13	333	12.0	452 2 B72387	hypothetical prote
14	304.5	10.9	458 2 B70145	aminopeptidase I

RESULT 1

A33879
aminopeptidase yaci (EC 3.4.11.-) precursor, vacuolar - yeast (Saccharomyces cerevisiae)
C#Alternate names: protein YKL03c; protein YKL455
C#Species: Saccharomyces cerevisiae
C#Date: 30-Sep-1991 #Sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C#Accession: A33879; B33879; S39101; S37330; S25400
R.Chang, Y.H.; Smith, J.A.
J. Biol. Chem. 264, 6979-6983, 1989
A#Title: Molecular cloning and sequencing of genomic DNA encoding aminopeptidase I from yeast 9, 1959-1965, 1993
A#Reference number: A33879; MUID:89214116; PMID:2651436
A#Accession: A33879
A#Molecule type: DNA
A#Residues: 1-514 <CIR>
A#Cross-references: UNIPROT:P14904; EMBL:M25548; NID:9295617; PID:AAA34738.1; PID:9295617
A#Accession: B33879
A#Molecule type: protein
A#Residues: 46-63 <CIR>
R.Cheret, G.; Pallier, C.; Valans, M.; Daignan-Fournier, B.; Fukuhara, M.; Bolotin-Fukuhara, M.; Daignan-Fournier, B.; Pallier, C.; Pu, A#Title: The DNA sequence analysis of the HAP2-LAP2 region on chromosome XI of Saccharomyces cerevisiae. A reference sequence for the HAP2-LAP2 region on chromosome XI of yeast 9, 1959-1965, 1993
A#Reference number: S39094; MUID:94152173; PMID:8109175
A#Accession: S39101
A#Status: translation not shown
A#Molecule type: DNA
A#Residues: 1-514 <CIR>
A#Cross-references: EMBL:X71133; NID:9431205; PID:CAA50454.1; PID:9431213
A#Experimental source: strain S288C
R.Cheret, G.; Fukuhara, M.; Daignan-Fournier, B.; Pallier, C.; Pu, A#Title: The DNA sequence analysis of the HAP2-LAP2 region on chromosome XI of Saccharomyces cerevisiae. A reference sequence for the HAP2-LAP2 region on chromosome XI of yeast 9, 1959-1965, 1993
A#Reference number: S37920
A#Accession: S37930
A#Molecule type: DNA
A#Residues: 1-514 <CIR>
A#Cross-references: EMBL:228103; NID:9486172; PID:CAA81943.1; PID:9486173; MIPS YKL10
A#Experimental source: strain S288C
R.Cueva, R.; Garcia-Alvarez, N.; Suarez-Rendueles, P.
BBBS Lett. 259, 125-129, 1989